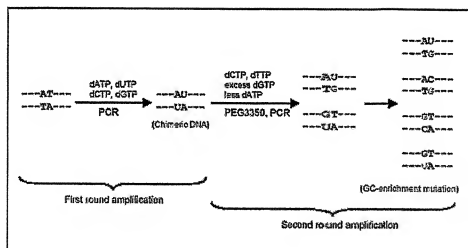


Figure 1



5

Figure 2

	34	38	41		103	105	107
AlbD	-R C I L F A A G L S G	- - - G V G H S L G S V-					
Bhc	-R A V L L L H G F T G	- - - V S G L S L G G V-					
Sac	-R A V L L L H G F T G	- - - V R G L S L G G D-					
Lic	-R A V L L L H G F T G	- - - I I G F S M G G V-					
Bsc	-K A V L L L H G F T G	- - - A C G L S L G G V-					
Tne	-K G V L F I H G Y T G	- - - I I G F S M G G V-					
Tpc	-K A V L L I H G Y K G	- - - V G G L S M G G V-					
Pcl	-Y P I I L Y K G L C G	- - - L V G H S Q G G Q-					
Bso	-A P L V L L H G F T G	- - - I I A H S Q G G Q-					
Consensus	L x x x G x x G	G x s x G					
	(I)	(A)					
	(V)						

**Figure 3**

MDKSDLTETSRIKHGEEAFDVTLLQVKGATRCILFAAGLGGSPLRHLELLQ  
TFARHGVSVVAPHFERLTSPVPTRAELLERCQRLARAQNEFCSGYASVTGV  
5 GHSLGSVILLNAGAIAMTSAGESVVFAGDRMLHRLILLAPPADFFQAPSA  
LAAVNVFVHIWAGEKDSLTPPSQACFLKQALEGYTQTYLCVMEEAGHFTFM  
NTLPPQVTDSPHSREAFLLDLGENIARLVTD

**Figure 4**

10 ATGGACAAAAGTGATCTCACGGAAACGTCTCGGATCAAACATGGGGAAGAG  
GCGTTTGACGTACCTTATTGCAGGTTAAGGGGGCGACGCGCTGTATCCTT  
TTTGCTGCGGGGCTGGGCGGCAGTCCGCTGCGCCATCTTGAACCTTCCAG  
ACCTTTGCCCCGCATGGCGTTTCCGTTGTCGCGCCACACTTTGAACGGTTG  
15 ACCTCACCCGTGCCCACCAGAGCTGAATTACTGGAACGCTGCCAGCGGCTT  
GCGCGGGCTCAGAATGAATTTTGTAGCGGTTATGCGTCGGTTACCGGTGTT  
GGCCACTCCCTGGGTAGCGTGATTTTATTGCTGAATGCCGGGGCTATAGCG  
ATGACAAGCGCAGGGGAATCGGTTGTTTTGCGCGGCGACCGGATGTTGCAT  
CGACTTATTTTACTGGCACCGCCCGCGGATTTTTTCCAGGCTCCGTCTGCG  
20 CTGGCAGCGGTGAACGTACCTGTTACATCTGGGCAGGTGAAAAGGACAGC  
CTGACGCCCCGTCCCAGGCCTGCTTTCTTAAACAGGCACTGGAGGGTTAC  
ACGCAGACTTATCTCTGTGTGATGGAAGAGGCCGGGCATTTTACCTTCATG  
AATACCTTGCCCTCCGCAGGTAACCGATTACATCCGTGCGGGGAGGCCTTT  
CTTTTAGATTTGGGCGAAAACATAGCCCGGCTGGTGACTGAT